

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2003, 14:50:12 ; Search time 41 Seconds

(without alignments)  
1951.129 Million cell updates/sec

Title: US-09-831-805A-6

Perfect score: 1635

Sequence: 1 MALRRPPLRLCARLPDFLL.....VNYINTDEGRFRHKSFVI 310

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_vertibrate.\*

14: sp\_unclassified.\*

15: sp\_rvirus.\*

16: sp\_bacteriap.\*

17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1629	99.6	310	4	Q9BX67
2	1629	99.6	355	4	Q8WVL8
3	1620	99.1	309	4	Q96FL1
4	1417	86.7	310	11	Q9D8B7
5	1415	86.5	310	11	Q9EPK4
6	1403	85.8	310	11	Q9DLM9
7	481.5	29.4	298	11	Q9J159
8	481.5	29.4	298	11	Q8C5K9
9	478.5	29.3	298	11	Q8CE95
10	458.5	28.0	300	11	Q9JHY1
11	449.5	27.5	300	11	Q9VC39
12	331	20.2	259	4	Q9Y5B2
13	321	19.6	173	11	Q9JKD5
14	291	17.8	64	11	Q8BT59
15	248	15.2	318	13	Q91664
16	242.5	14.8	304	11	Q9CVA4

17	241	14.7	327	4	Q96IQ7	Q96iq7 homo sapien
18	239.5	14.6	284	4	Q9NX42	Q9nx42 homo sapien
19	239.5	14.6	325	4	Q95791	Q95791 homo sapien
20	232.5	14.2	328	11	Q9Z109	Q9z109 mus musculus
21	221.5	13.5	319	11	Q922D5	Q922d5 mus musculus
22	215.5	13.2	319	11	Q9JKA5	Q9jka5 mus musculus
23	215	13.1	407	11	Q9DZJ4	Q9dzj4 mus musculus
24	209.5	12.8	335	13	Q9PWR4	Q9pwr4 gallus gall
25	209	12.8	181	13	Q91665	Q91665 xenopus lae
26	206.5	12.6	335	13	Q9YGH1	Q9ygh1 gallus gall
27	205.5	12.6	248	11	Q9D0T4	Q9d0t4 mus musculus
28	201.5	12.3	335	13	Q9YGV5	Q9ygv5 gallus gall
29	199.5	12.2	372	13	Q90Y50	Q90y50 brachydanio
30	197.5	12.1	373	4	Q9H6B4	Q9h6b4 homo sapien
31	193.5	11.8	795	13	Q90YMO	Q90ymo brachydanio
32	189	11.6	259	4	Q95532	Q95532 homo sapien
33	187	11.4	725	13	Q73633	Q73633 xenopus lae
34	186.5	11.4	358	13	Q90490	Q90490 brachydanio
35	184.5	11.3	838	13	Q90YML	Q90yml brachydanio
36	182.5	11.2	372	11	Q8K1G0	Q8k1g0 rattus norv
37	182.5	11.2	1409	13	Q8J127	Q8j127 brachydanio
38	182.5	11.2	1428	13	Q8AY67	Q8ay67 brachydanio
39	180.5	11.0	1894	11	Q64487	Q64487 mus musculus
40	180	11.0	344	5	Q8WR42	Q8wr42 caenorhabdi
41	180	11.0	345	5	Q8MPV0	Q8mpv0 caenorhabdi
42	180	11.0	435	5	Q8WR44	Q8wr44 caenorhabdi
43	180	11.0	436	5	Q8MPV1	Q8mpv1 caenorhabdi
44	180	11.0	443	5	Q8WR43	Q8wr43 caenorhabdi
45	180	11.0	444	5	Q8MPU9	Q8mpu9 caenorhabdi

## ALIGNMENTS

RESULT 1

Q9BX67 PRELIMINARY; PRT; 310 AA.

AC Q9BX67;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Junctional adhesion molecule 3 precursor (Junctional adhesion molecule-2) (Junctional adhesion molecule-3) (Hypothetical protein FLJ90288) (Hypothetical protein FLJ90828).  
GN JAM-2 OR JAM3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Cunningham S.A., Arrate M.P., Tran T.M.;  
RT "Cloning of Human Junctional Adhesion Molecule 3.";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Aurrand-Lions M.A., Johnson-leger C., Wong C., Dupasquier L.;  
RT "Heterogeneity of endothelial junctions is reflected by differential expression and specific subcellular localization of the three JAM family members.";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;  
RT "Junctional adhesion molecules (JAMs) and interendothelial junctions.";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Sachs U.J.H., Eva O., Berghoefer H., Santos S.;  
RT "Characterization of Junctional Adhesion Molecule-3 on Human Platelets: A New Member of Immunoglobulin Superfamily.";

```

RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.,
RT "NEDO human cDNA sequencing project.",
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF356518; AAK27221.1; -.
DR EMBL; AJ344431; AAC69845.1; -.
DR EMBL; AF448478; CAM20925.1; -.
DR EMBL; AK074769; BAC11195.1; -.
DR EMBL; AK075309; BAC11538.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
KW Hypothetical protein; Signal.
FT SIGNAL 1 30
FT SEQUENCE 310 AA; 35020 MW; CE39ADF33BA1DAB9 CRC64;
SQ SEQUENCE 310 AA; 35020 MW; CE39ADF33BA1DAB9 CRC64;

Query Match 99.6%; Score 1629; DB 4; Length 310;
Best Local Similarity 99.7%; Pred. No. 2.2e-152;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTVPVQEFSEVLSCTITDSQT 60
DB 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTVPVQEFSEVLSCTITDSQT 60

QY 61 SDPRIWKKIODEQTYVFFDNKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVVAR 120
DB 61 SDPRIWKKIODEQTYVFFDNKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVVAR 120

QY 121 NDRKEIDEIVELTVQVKPVPVCRVPAVPGKMATLHCQSEGHPRPHYSWYRNDVPL 180
DB 121 NDRKEIDEIVELTVQVKPVPVCRVPAVPGKMATLHCQSEGHPRPHYSWYRNDVPL 180

QY 181 PTDSRANPRFRNSSHLNSETGLVFTAVHKDDSGQYICIASNDAGSARCEQEVEVDL 240
DB 181 PTDSRANPRFRNSSHLNSETGLVFTAVHKDDSGQYICIASNDAGSARCEQEVEVDL 240

QY 241 NIGGIIGVLVLAVALITLIGICAYRRGYFINNKQGESYKPKGPDGVNYIRTDDEG 300
DB 241 NIGGIIGVLVLAVALITLIGICAYRRGYFINNKQGESYKPKGPDGVNYIRTDDEG 300

QY 301 DFRHKSSPVI 310
DB 301 DFRHKSSPVI 310

RESULT 2
Q8WNL8 PRELIMINARY; PRT; 355 AA.
AC Q8WNL8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Junction adhesion molecule 3.
GN JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RT "Narrowing the critical region within 11q24-qter for hypoplastic left

RT heart and identification of a candidate gene, JAM3, expressed during
RT cardiogenesis.";
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416101; CAC94776.1; -.
DR Genew; HGNC:15532; JAM3.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 2.
KW Immunoglobulin domain.
FT CHAIN 76 355
FT SEQUENCE 355 AA; 39602 MW; 8B1577DEA7B1D4F8 CRC64;

Query Match 99.6%; Score 1629; DB 4; Length 355;
Best Local Similarity 99.7%; Pred. No. 2.7e-152;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTVPVQEFSEVLSCTITDSQT 60
DB 46 MALRRPRLRLCARLPDFFLLFRGCLIGAVNLKSSNRTVPVQEFSEVLSCTITDSQT 105

QY 61 SDPRIWKKIODEQTYVFFDNKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVVAR 120
DB 106 SDPRIWKKIODEQTYVFFDNKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVVAR 165

QY 121 NDRKEIDEIVELTVQVKPVPVCRVPAVPGKMATLHCQSEGHPRPHYSWYRNDVPL 180
DB 166 NDRKEIDEIVELTVQVKPVPVCRVPAVPGKMATLHCQSEGHPRPHYSWYRNDVPL 225

QY 181 PTDSRANPRFRNSSHLNSETGLVFTAVHKDDSGQYICIASNDAGSARCEQEVEVDL 240
DB 226 PTDSRANPRFRNSSHLNSETGLVFTAVHKDDSGQYICIASNDAGSARCEQEVEVDL 285

QY 241 NIGGIIGVLVLAVALITLIGICAYRRGYFINNKQGESYKPKGPDGVNYIRTDDEG 300
DB 286 NIGGIIGVLVLAVALITLIGICAYRRGYFINNKQGESYKPKGPDGVNYIRTDDEG 345

QY 301 DFRHKSSPVI 310
DB 346 DFRHKSSPVI 355

RESULT 3
Q96FL1 PRELIMINARY; PRT; 309 AA.
AC Q96FL1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010690; AAH10690.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 2.
KW Hypothetical protein; Immunoglobulin domain.
FT NON_TER 1
FT SEQUENCE 309 AA; 34917 MW; 50C5B1B7872E8DF3 CRC64;

Query Match 99.1%; Score 1620; DB 4; Length 309;
```

Best Local Similarity 99.4%; Pred. No. 1.7e-151;  
Matches 307; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ALRRPRLRLCARLPDFLLFRGLIGAVNLKSSNRPVVOEFESVELSCIITDSQTS 61  
DB 1 ALRRPRLRLCARLPDFLLFRGLIGAVNLKSSNRPVVOEFESVELSCIITDSQTS 60

QY 62 DPRIEWKIKQDEQTTTFFDNKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVARN 121  
DB 61 DPRIEWKIKQDEQTTTFFDNKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVARN 120

QY 122 DRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 181  
DB 121 DRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180

QY 182 TDSRANPRFRNSSHLNSETGLVFTAVHKDDSGQYICIASNDAGSARCEQEMEYVDLN 241  
DB 181 TDSRANPRFRNSSHLNSETGLVFTAVHKDDSGQYICIASNDAGSARCEQEMEYVDLN 240

QY 242 IGGIIGVVLVLAVALITLIGICCAIRRGYFNNKQDGESYKXNPKGPDGVNVRTDEGD 301  
DB 241 IGGIIGVVLVLAVALITLIGICCAIRRGYFNNKQDGESYKXNPKGPDGVNVRTDEGD 300

QY 302 FRHKSSEVI 310  
DB 301 FRHKSSEVI 309

RESULT 4  
Q9DB87 ID Q9DB87 PRELIMINARY; PRT; 310 AA.  
AC Q9DB87  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-WAR-2003 (TRENBLrel. 23, Last annotation update)  
DE 1110002N23rik protein.  
GN JCAM3 OR JCAM2 OR 1110002N23RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Small intestine;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzaletti J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL; AK008187; BAB25519.1; -.  
DR MGD; MGI:1933820; Jcam3.  
DR MGD; MGI:1933825; Jcam3.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG-c2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; IG; 2.  
DR SMART; SM00408; IGC2; 1.

DR PROSITE; PS50835; IG\_LIKE; 2.  
KW Immunoglobulin domain.  
SQ SEQUENCE 310 AA; 34855 MW; C74884EABE234680 CRC64;

Query Match 86.7%; Score 1417; DB 11; Length 310;  
Best Local Similarity 86.1%; Pred. No. 2e-131;  
Matches 267; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

QY 1 MALRRPRLRLCARLPDFLLFRGLIGAVNLKSSNRPVVOEFESVELSCIITDSQTS 60  
DB 1 MALRRPRLRLCARLPDFLLFRGLIGAVNLKSSNRPVVOEFESVELSCIITDSQTS 60

QY 61 SDPRIEWKIKQDEQTTTFFDNKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVARN 120  
DB 61 SDPRIEWKIKQDEQTTTFFDNKIQGLAGRAEILGKTSLKINWTRRDSALYRCEVARN 120

QY 121 NDRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180  
DB 121 NDRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180

QY 181 PTDSRANPRFRNSSHLNSETGLVFTAVHKDDSGQYICIASNDAGSARCEQEMEYVDL 240  
DB 181 PTDSRANPRFRNSSHLNSETGLVFTAVHKDDSGQYICIASNDAGSARCEQEMEYVDL 240

QY 241 NIGGIIGVVLVLAVALITLIGICCAIRRGYFNNKQDGESYKXNPKGPDGVNVRTDEBG 300  
DB 241 NIGGIIGVVLVLAVALITLIGICCAIRRGYFNNKQDGESYKXNPKGPDGVNVRTDEBG 300

QY 301 DFRHKSSEVI 310  
DB 301 DFRHKSSEVI 310

RESULT 5  
Q9EPK4 ID Q9EPK4 PRELIMINARY; PRT; 310 AA.  
AC Q9EPK4  
DT 01-MAR-2001 (TRENBLrel. 16, Created)  
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Functional adhesion molecule-2, JAM-2 (1110002N23rik protein)  
DE (Junction cell adhesion molecule 3).  
GN JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Embryo;  
RX PubMed=11036763;  
RA Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;  
RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular  
RL Family?";  
RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Embryo;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzaletti J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;  
RX MEDLINE=22354683; PubMed=12466851;  
RA Straussberg R.;  
RL Submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.  
RV [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Mesonephros;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
DR EMBL; AJ300304; CAC20704.1; -;  
DR EMBL; AK013156; BAB28683.1; -;  
DR EMBL; BC024357; BAH24357.1; -;  
DR EMBL; AK032833; BAC28049.1; -;  
DR MGD; MGI:1933820; Jcam2.  
DR MGD; MGI:1933825; Jcam3.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; ig; 2.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS0835; IG\_LIKE; 2.  
KW Immunoglobulin domain.  
SQ SEQUENCE 310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;  
  
Query Match 86.5%; Score 1415; DB 11; Length 310;  
Best Local Similarity 86.1%; Pred. No. 3.1e-131;  
Matches 267; Conservative 18; Mismatches 25; Indels 0; Gaps 0;  
  
QY 1 MALRPPRLRLCARLPDPFLLLLFRGLIGAVLNKSSNRTPVQVFESVELSCIITDSQT 60  
DB 1 MALSRLRLRLYARLPDPFLLLLFRGCMIEAVLNKSSNRPVHFEFVELSCIITDSQT 60  
  
QY 61 SDPIEWKKIQDEQTYVFFDNKIQDLAGRAEILGKTSKIWNVTRRDSALYRCEVVAR 120  
DB 61 SDPIEWKKIQDQTYVFFDNKIQDLAGRTDVFGLTSLRINWVTRSDSALYRCEVVAL 120  
  
QY 121 NDRKEIDEIVLTVOVKPVPVCRPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180  
DB 121 NDRKEVEDEITIELIVQVKPVPVCRIPAAVPVGKTATLQCQSEGYPRPHYSWYRNDVPL 180  
  
QY 181 PTDSRANPRFRNSSHLNSETGLVFTAVHKDDSGQYICIASNDAGSARCEQMEVYDL 240  
DB 181 PTDSRANPRFQNSFHVNSETGLVFNVAHKDDSGQYICIASNDAGARCEQDMEVYDL 240  
  
QY 241 NIGGIIGVVLVAVLALITLIGICCAIRRGYFINKKQGESYKPKGPDGVNYIRTDSEEG 300  
DB 241 NIAGIIGVVLVAVLAVITMGICCAIRRGYFINKKQGESYKSGKDHGVNYIRTDSEEG 300  
  
QY 301 DFRHKSFFVI 310  
DB 301 DFRHKSFFVI 310  
  
RESULT 6  
Q9D1M9 PRELIMINARY; PRT; 310 AA.  
AC Q9D1M9;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE I110002N23rik protein.  
GN JCAM3 OR JCAM2 OR I110002N23RIK.  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Embryo;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Arizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,  
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL; AK003326; BAB22715.1; -;  
DR MGD; MGI:1933820; Jcam2.  
DR MGD; MGI:1933825; Jcam3.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; ig; 2.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS0835; IG\_LIKE; 2.  
KW Immunoglobulin domain.  
SQ SEQUENCE 310 AA; 34819 MW; 6692BCAD68EA4B1D CRC64;  
  
Query Match 85.8%; Score 1403; DB 11; Length 310;  
Best Local Similarity 85.2%; Pred. No. 4.7e-130;  
Matches 264; Conservative 20; Mismatches 26; Indels 0; Gaps 0;  
  
QY 1 MALRPPRLRLCARLPDPFLLLLFRGLIGAVLNKSSNRTPVQVFESVELSCIITDSQT 60  
DB 1 MALSRLRLRLYARLPDPFLLLLFRGCMIEAVLNKSSNRPVHFEFVELSCIITDSQT 60  
  
QY 61 SDPIEWKKIQDEQTYVFFDNKIQDLAGRAEILGKTSKIWNVTRRDSALYRCEVVAR 120  
DB 61 SDPIEWKKIQDQTYVFFDNKIQDLAGRTDVFGLTSLRINWVTRSDSALYRCEVVAL 120  
  
QY 121 NDRKEIDEIVLTVOVKPVPVCRPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPL 180  
DB 121 NDRKEVEDEITIELIVQVKPVPVCRIPAAVPVGKTATLQCQSEGYPRPHYSWYRNDVPL 180  
  
QY 181 PTDSRANPRFRNSSHLNSETGLVFTAVHKDDSGQYICIASNDAGSARCEQMEVYDL 240  
DB 181 PTDSRANPRFQNSFHVNSETGLVFNVAHKDDSGQYICIASNDAGARCEQDMEVYDL 240  
  
QY 241 NIGGIIGVVLVAVLALITLIGICCAIRRGYFINKKQGESYKPKGPDGVNYIRTDSEEG 300  
DB 241 NIAGIIGVVLVAVLAVITMGICCAIRRGYFINKKQGESYKSGKDHGVNYIRTDSEEG 300  
  
QY 301 DFRHKSFFVI 310  
DB 301 DFRHKSFFVI 310  
  
RESULT 7  
Q9J159 PRELIMINARY; PRT; 298 AA.  
ID Q9J159  
AC Q9J159;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

```
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vascular endothelial junction-associated molecule (Junctional adhesion
DE molecule-3) (241003OG21RIK protein).
GN JCAM3 OR JCAM2 OR JAM-3 OR 241003OG21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20317114; PubMed=10779521;
RT Palmeri D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.;
RT "Vascular Endothelial Junction-associated Molecule, a Novel Member of
RT the Immunoglobulin Superfamily, Is Localized to Intercellular
RT Boundaries of Endothelial Cells.";
RL J. Biol. Chem. 275:19139-19145 (2000).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX PubMed=11036763;
RA Aurand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT Family";
RL Curr. Top. Microbiol. Immunol. 251:91-98 (2000).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic stem cells;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaaszerland T., Glessi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
DR EMBL; AF255911; AAF81224.1; -
DR EMBL; AJ291757; CAC20699.1; -
DR EMBL; AK013914; BAB29053.1; -
DR EMBL; AK010616; BAB27064.1; -
DR MGD; MGI:1933820; Jcam2.
DR MGD; MGI:1933825; Jcam3.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; igf; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 33047 MW; 1124E0F07B6CF751 CRC64;

Query Match 29.4%; Score 481.5; DB 11; Length 298;
Best Local Similarity 36.7%; Pred. No. 4.7e-39;
Matches 114; Conservative 53; Mismatches 117; Indels 27; Gaps 9;

QY 13 ARLPDFFLLPRGLGICAVNLKSN-----RTPVQEFESVELSCIITDSQTSDP 63
D 1 ARSPQGLMLLLHYLVALDYHKANGFSASKDHQEVTVIEFQAILAC-KTPKKTSS 60
QY 64 RIEWKKIQDEQTYVFFDNKIQGLAGRAELIGKTSIKWNVTRDSALYRCVVARND 123
D 1 RLEWKV-QGGVSLVYQQALQGFQKRAEMI-DENIRIKNVTSDAGEYRCVSAPT 118
QY 124 -KEIDEIVIELTVQKPVTPVCRVPKAVPVGKMATLHCQSEGHPRPHYSYRNDV 182
D 1 GQNLEQDKWLEVLVAPVAPACEVPTSVMTGVSVELRCQDKEGNPAPEYIWFK 176
QY 183 DSRANPR---NSSSHLNSETGLVFTAVHKDSDGQYCIASNDAGSARCEQE 239
D 1 --LGNPKGRTHNNSYTMNTKSGILQFNMIKSDSGEYICARNVSGHRRCPG 234
QY 240 LNIIGIGGVVLAVLALITLIGCCAVRRGYFNNKQDGSYKPNKPGKPDGVN 299
D 1 LNIIGIGGVVLAVLALITLIGCCAVRRGYFNNKQDGSYKPNKPGKPDGVN 299
QY 300 GDFRHKSSFVI 310
D 1 NDFKHTKSFII 298

RESULT 9
ID Q8CE95 PRELIMINARY; PRT; 298 AA.

QY 124 -KEIDEIVIELTVQKPVTPVCRVPKAVPVGKMATLHCQSEGHPRPHYSYRNDV 182
D 1 GQNLEQDKWLEVLVAPVAPACEVPTSVMTGVSVELRCQDKEGNPAPEYIWFK 176
QY 183 DSRANPR---NSSSHLNSETGLVFTAVHKDSDGQYCIASNDAGSARCEQE 239
D 1 --LGNPKGRTHNNSYTMNTKSGILQFNMIKSDSGEYICARNVSGHRRCPG 234
QY 240 LNIIGIGGVVLAVLALITLIGCCAVRRGYFNNKQDGSYKPNKPGKPDGVN 299
D 1 LNIIGIGGVVLAVLALITLIGCCAVRRGYFNNKQDGSYKPNKPGKPDGVN 299
QY 300 GDFRHKSSFVI 310
D 1 NDFKHTKSFII 298

RESULT 9
ID Q8CE95 PRELIMINARY; PRT; 298 AA.
```



```
QY 75 TTYVFFDNKIQDLAGRAEILGKTSKIWNVTRDSALYRCVWARNDRKEIDEIVIELT 134
Db 69 TALVCYNSQITAPYADRV-TFSSGITTSSVTRKONGEYTC-MVSEGGQNYGEVSIHLT 126
QY 135 VOVKPVTPVCRVPKAVPGKMATLHCQSEGHPRPHYSWYRNDVPLPT-DSRANPRFRNS 193
Db 127 VLVPPSKPTISVPSSVTIGNRAVLTCSEHDSPPSEYFWKDGISMLTADAKKTRAFMNS 186
QY 194 SSSLNSETGTLVFTAVHKDDSQYYCIASNDAGSA-RCEEQMEVYDNLNIGLIGGLVW 252
Db 187 SFTIDPKSGDLIFDFTAFDSEYICQAGNGYGTAMRSEAAHMDAVELNVGGIVAAVLVT 246
QY 253 LAVLALITLIGICAYRRGYFFINNKDGESYKPNKPGDGVNVRTDEEGDFRHKSSFVI 310
Db 247 LILLGLLIFGVWFAYSRGVFERTKKG----TAPGKKVIYSQPSRSEGEFKQTSSEFLV 300

RESULT 12
QY5B2
ID Q9Y5B2 PRELIMINARY; PRT; 259 AA.
AC Q9Y5B2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Junctional adhesion molecule.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Liu Y., Nusrat A., Schnell F.J., Walsh S., Reeves T.A., Pochet M.,
RA Foley C., Parkos C.A.;
RT "Human junctional adhesion molecule is expressed by polarized columnar
RT epithelia and regulates tight junction resealing.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF154005; AAD43794.1; -.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin domain.
KW Immunoglobulin domain.
SQ SEQUENCE 259 AA; 28122 MW; FE38521A911582D0 CRC64;

Query Match 20.2%; Score 331; DB 4; Length 259;
Best Local Similarity 29.6%; Pred. No. 2.9e-24;
Matches 81; Conservative 44; Mismatches 111; Indels 38; Gaps 7;

QY 42 VQVESEVELSCIITDSQTSQPIBWKIODEQTYVFFDNKIQDLAGRAEILGKTSLK 101
Db 19 ILPENPNVKLSQAY--SGFSGR---AASDVRVTL-----PTGIT 55
QY 102 IWNVTRDSALYRCVWARNDRKEIDEIVIELTVQKVPVCRVPKAVPGKMATLHCQ 161
Db 56 FKSVRTETGIYTC-MVEEGGNSYGEVKVLIIVLPESKPTVNIPTSSATIGNRAVLTC 114
QY 162 ESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSLNSETGTLVFTAVHKDDSQYYCIA 221
Db 115 EQDGSPPEYTWFKDGIWMTPNPKSTRAFSNYSVNLNPTTGLVFDPLSADTGEYSCEA 174
QY 222 SNDAGSARCEQ-EDEVYDNLNIGLIGGLVWVLAVALITLIGICAYRRGYFFINNKDGE 280
Db 175 RNVGYTPTMSTNAVRMEARNVGVVAAVLVLLILLGLVFGVWFAYSRGVFERTKKGTS 234
QY 281 S----YKNPGRPGDGVNVRTDEEGDFRHKSSFVI 310
Db 235 SKKVIYSQPS-----ARSEGEFKQTSSEFLV 259

RESULT 13
```

```
Q9JKD5
ID Q9JKD5 PRELIMINARY; PRT; 173 AA.
AC Q9JKD5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Junctional adhesion molecule (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RA Kirsch T., Wellner M., Haller H., Lippoldt A.;
RT "Cloning of the rat junctional adhesion molecule (JAM).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF241261; AAF61729.1; -.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin domain.
KW NON TER
FT NON TER 1
SQ SEQUENCE 173 AA; 18706 MW; 3EE3ECDFA5AFB8B2 CRC64;

Query Match 19.6%; Score 321; DB 11; Length 173;
Best Local Similarity 40.3%; Pred. No. 1.6e-23;
Matches 71; Conservative 27; Mismatches 72; Indels 6; Gaps 3;

QY 137 VKPVTVPVCRVPKAVPGKMATLHCQSEGHPRPHYSWYRNDVPLPT-DSRANPRFRNS 195
Db 2 VPPSKPTVSPSSVTIGNRAVLTCSEHDSPPSEYFWKDGVPMLTADAKKTRAFINSSY 61
QY 196 HLNSETGTLVFTAVHKDDSQYYCIASNDAGSA-RCEEQMEVYDNLNIGLIGGLVWVLA 254
Db 62 TIDPKSGDLVFDVPVSAPDSGEYCEAQNGYGTAMRSEAVRMEAVELNVGGIVAAVLTLI 121
QY 255 VLALITLIGICAYRRGYFFINNKDGESYKPNKPGDGVNVRTDEEGDFRHKSSFVI 310
Db 122 LLGLLIFGVWFAYSRGVFERTKKG----TAPGKKVIYSQPSRSEGEFKQTSSEFLV 173

RESULT 14
Q8BT59
ID Q8BT59 PRELIMINARY; PRT; 64 AA.
AC Q8BT59;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Junction cell adhesion molecule 3 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN=CS7BL/6J; TISSUE=Body;
RC MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK01692; BAC25526.1; -.
FT NON TER 1
SQ SEQUENCE 64 AA; 6996 MW; AF46BC30AA6D0C11 CRC64;

Query Match 17.8%; Score 291; DB 11; Length 64;
Best Local Similarity 85.9%; Pred. No. 3.8e-21;
Matches 55; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
```

